Transcriptome analysis of tobacco in response to *Ralstonia solanacearum* infection

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**Abstract:** One of the best strategies to control bacterial wilt caused by *Ralstonia solanacearum* (Smith) is generally based on breeding resistant cultivars. The information obtained from the expression of plant defense genes will provide new insight for improving plant resistance against pathogens. This study was to identify inducible genes under defense no death (DND) reaction of tobacco (*Nicotiana tabacum*)-*R. solanacearum* interaction using cDNA-AFLP technique. In this assay five different primer combinations were used. Out of 1320 Transcript derived fragments (TDF) that were detected, 101 fragments were identified as differentially expressed genes in 0, 24, 48 and 72 hours post inoculation. Most of the differentially expressed genes were obtained 48 hours post inoculation. Following sequencing, most of sequenced TDFs showed homology to known genes interfering in signaling, regulation and defense functions. DND phenotype in tobacco has some similarities specially in signaling process with mechanism associated with induction of the hypersensitive reaction and it is distinct from general defense mechanisms.

**Keyword:** Tobacco, *Ralstonia solanacearum*, transcriptome, interaction

**Introduction**

The phytopathogenic bacterium *Ralstonia solanacearum* is a devastating, soil-borne pathogen that causes lethal wilting of plants in over 200 species (Hayward, 1991; Buddenhagen and Kelman, 1964). The strategy to control bacterial wilt is generally based on breeding resistant cultivars, while other preventive methods are difficult to apply (Carputo and Barone, 2005).

During plant-pathogen interactions gene expressions are altered and defense mechanisms activated or suppressed. When Plants are exposed to pathogens attack, compatible interaction occurs via colonizing susceptible plant with pathogen and under incompatible interaction defense mechanisms stimulate and prevent pathogen entry, establishment and growth in the plant (Kamoun, 2001; Thordal-Christensen, 2003; Daurelio *et al.*, 2009 a, b).

Elicitation of hypersensitive reaction (HR) as incompatible reaction occurs by leaf infiltration with rich bacterial suspension and rapid necrosis of plant cells in infection site has been observed 12-24 hours post inoculation (Carney *et al.*, 1990; Klement, 1982). In compatible interaction, bacteria multiply for a prolonged period and
water soaked lesions appear nearly 3 days after inoculation (Lozano and Sequeira, 1970). Race 3 of \textit{R. solanacearum} isolates induce defense no death reaction but don’t induce HR on tobacco (OEPP/EPPO, 1990). The bacteria unable to spread into adjacent tissues and cause chlorotic reaction. The factors responsible for this resistance may be different from HR (Lozano and Sequeira, 1970). Race 3 of \textit{R. solanacearum} isolates is the prevalent race in potato production sites in Iran (Nouri et al., 2009). The level of resistance in cultivated potato varieties is low and crossing of Solanum species is time-consuming and hard, therefore the development of resistant genotypes has become a challenge for potato breeders (Carputo et al., 2009).

Generally, investigation on tobacco molecular responses against \textit{R. solanacearum} may be assisted by transferring desirable defense genes to \textit{S. tuberosum} cultivars using genetic engineering methods.

Defense mechanisms and induced responses in the various host and non host/\textit{R. solanacearum} interactions have been studied previously (Dahal et al., 2009; Schacht et al., 2011; Kiba et al., 2007; Godiard et al., 1990; Gao et al., 2009; Esposito et al., 2009).

Natural invasion of \textit{R. solanacearum} occurs through the root system and after heavy colonization of the vascular tissues, wilting symptoms appear (Vasse et al., 1995). Leaf infiltration technique, is more accurate in comparison to root inoculation and has been suggested for studying molecular aspects of Tobacco/\textit{R. solanacearum} interactions (Kiba et al., 2007).

Transcriptome analysis of incompatible response (non-host or avirulent) in tobacco and \textit{R. solanacearum} (race 3) interaction will provide new insights for improving plant resistance against pathogens and for effective control of bacterial wilt disease. Information on the defense mechanisms and genes involved in plant-pathogen interactions would be highly desirable and necessary. This study is conducted to identify inducible genes in interaction of tobacco against \textit{R. solanacearum} by leaf-infiltration using cDNA-AFLP method.

**Materials and Methods**

**Plant material and bacterial inoculation procedure**

\textit{Nicotiana tabacum} cv. Samsun (Seed obtained from Seed and Plant Improvement Institute, Iran), were grown in pots containing a mixture of vermiculite-peat moss (3:1) under controlled greenhouse conditions at 25 °C and 10000 lux with a photoperiod of 16h. Forty days old tobacco plants were used for leaf infiltration. The bacterial strain (SH12) used in this study was \textit{R. solanacearum} race3/biovar2 isolated from potato in Khuzestan province. Culture of bacteria were routinely grown (24h, 28 °C) on yeast peptone glucose agar (YPGA) medium. Bacterial suspension of $10^8$ CFU/ml (0.1 at OD600) from overnight bacterial culture was pressure infiltrated into the abaxial side of the leaves using a syringe without needle. Inoculated regions were harvested at 0, 24, 48 and 72 hours post inoculation (hpi). Water infiltrated leaves were used as control at the first point time. Collected tissues were frozen in liquid nitrogen immediately after harvesting. Samples were prepared in four replicates.

**RNA isolation and cDNA synthesis**

Total RNA was extracted from infected and non-infected tobacco using RNeasy® mini kit (Qiagen), according to the manufacturer's protocol. The mRNA was purified from 200μg of total RNA using oligotex mRNA purification kit according to the manufacturer's instructions (Qiagen). The quantity and quality of total RNA and mRNA were examined on 1% agarose gel. First strand cDNA was synthesized using first strand cDNA synthesis kit according to the manufacturer's protocol (Fermentas).

Double stranded cDNA was synthesized by adding, 20 μl first-strand cDNA reaction to a master mix consisting of 7.5 μl of 10× cDNAII buffer, 25 U of DNA Polymerase I (Promega), 2.25 U of RNase H (Promega), and 1.25 μl dNTPs (10 mM) in a final volume of 80 μl, and incubating for 2h at 16 °C. The quality of double-stranded cDNA was determined by
electrophoresis on a 1% agarose gel. The remaining sample was purified by extraction with phenol/chloroform/isoamyl alcohol (1:1:24) and then ethanol precipitated.

cDNA-AFLP analysis

A cDNA-AFLP analysis was performed as described by Bachem et al. (1998). Transcript derived fragment (TDFs) were obtained after digestion of the dsDNA with 5U of MseI and EcoRI (invitogen). EcoRI and MseI adaptors were then ligated to the digested cDNA. Ten μL of the ligation mix and MseI and EcoRI primers without selective nucleotide were used for pre-selective amplification. In pre-amplification assay, PCR conditions in volume of 25 μl were as follow: 3 μl template cDNA (ligation product), 0.2 mM dNTP (10 mM), 1x PCR buffer, 1.5 mM MgCl₂, 1 U Taq polymerase and 0.4 μM of each primer (Mse0 and Eco0). The temperature profile for PCR amplification was 94 °C pre-denaturation for 3 min followed by 15 cycles of denaturation at 94 °C for 30 s, annealing at 56 °C for 1 min and extension at 72 °C for 1 min, and final extension at 72 °C for 5 min. After pre-amplification the mixture was diluted 50 fold and 3 μl was used for selective amplification with 5 primer combinations (MseAT/EcoCT, MseAT/EcoAC, MseCC/EcoCT, MseCC/EcoAC, MseAC/EcoAC). PCR conditions were the same as pre-amplification assay. Touchdown PCR conditions for selective amplification were as follows: 94 °C pre-denaturation for 1 min followed by denaturation at 94 °C for 30 s, annealing at 65 °C for 30 s and extension at 72 °C for 30 s. (12 cycles, scale down of 0.7 °C per cycle), 30 s denaturation at 94 °C, 30 s annealing at 56 °C, 60 s extension at 72 °C (23 cycle) and final extension at 72 °C for 5 min. Selective amplification products were resolved in a 8% denaturing polyacrylamide gel (Sequi-Gen GT sequencing cell of Bio-Rad) and running for 2.5h at 105 W and 50 °C. Polyacrylamide gel was visualized by silver staining (Bassam et al., 1991). TDFs of interest were excised from the gel. Each gel slice was immerged in 50 μl of sterile water and incubated overnight at 4 °C in order to allow the DNA fragments to diffuse. After centrifugation, the extracts were reamplified using AFLP selective primers under the same PCR conditions. PCR product was purified by Fermentas DNA extraction kit according to the manufacturer’s protocol then purified PCR products were sequenced. The nucleotide sequences were analyzed for homology against in Gen-Bank non-redundant database using Basic Local Alignment Search Tool (Blast) Program. Sequences were manually assigned to functional categories based on the analysis of scientific literature.

Result

Tobacco leaf reaction following bacterial infiltration

Isolate SH₁₂ induced severe chlorosis in the infiltrated area 48 h after infiltration (Table 1). The degree of chlorosis increased up to 72 h post inoculation but size of the lesion remained constant.

<table>
<thead>
<tr>
<th>Symptoms</th>
<th>HR</th>
<th>DND</th>
</tr>
</thead>
<tbody>
<tr>
<td>Restricted pathogen growth</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Spot color</td>
<td>brown</td>
<td>yellow</td>
</tr>
<tr>
<td>Appearance discoloration</td>
<td>24 hpi</td>
<td>48 hpi</td>
</tr>
</tbody>
</table>

hpi: hours post inoculation.

cDNA-AFLP analysis

The cDNA-AFLP strategy was successfully used to characterize differential gene expression under tobacco incompatible reaction against race 3 of *R. solanacearum* infiltration. The leaves were evaluated at different times after infection including 0, 24, 48 and 72 hour post inoculation (hpi). For five primer combinations, 1320 TDFs were visualized as bands, 50-800 bp in size. To determine reproducibility of these profiles, the experiments were repeated twice (Fig. 1).
Figure 1 cDNA-AFLP display using five primers combination (E, D, G, A and B) from water infiltrated leaves (lane c), pathogen infiltrated leaves that harvested at 24, 48 and 72 hours post inoculation (hpi). Arrows represent differential bands and magnifications show different expression patterns in control sample compared to pathogen infiltrated leaves.

From 1320 TDFs, 101 genes showed significantly different expression pattern in response to bacteria infiltration. Twenty four hours after infiltration many polymorphic fragments could be evidenced and most of them were up-regulated compared to control plant. 19.2% of cDNA-AFLP fragments corresponded to up regulated transcripts and 9.3% to down regulated transcripts (Fig. 2). Twenty of these cDNA fragments were excised from the gel and sequences were determined. The recovery from acrylamide gel and re-amplification was tricky step and thus we were not able to get a clean sequence for all cDNA fragments. Out of 20 sequences we obtained 11 clean sequences from stress responsive transcripts that showed a length between 79-159 bp (Table 2).

Figure 2 Overall results of cDNA-AFLP analysis in tobacco-Ralstonia solanacearum.
Bioinformatics' analyses were performed and TDFs classified in two groups with functional annotation and unknown function. The major function of deregulated genes was signaling, regulation and defense.

**Discussion**

Restriction of pathogen to its site of penetration is one of the plant defense strategies against pathogen. Defense No Death (DND) phenotype is induced in tobacco by race 3 of *Ralstonia solanacearum* (OEP/EPPO, 2004). A cDNA-AFLP approach was used to study transcriptome variation during *R. solanacearum*-tobacco interaction. This revealed the presence of metabolites generally expressed under stress conditions and which could be involved in the plant–pathogen incompatible reaction. Infiltration of suspension of *R. solanacearum* to tobacco leaves induced a condition similar to other stresses especially oxidative stress.

Generally when bacteria are introduced into plant tissues, defense gene activation may be more important than hypersensitive cell death in order to control pathogen growth (Jakobeck and Lindgran, 1993; Klement et al., 2003).

Ascorbate peroxidase (APX) (TE2) was shown to be induced under incompatible tobacco and *R. solanacearum* interaction. APX is a reactive oxygen species (ROSs) scavenging enzyme involved in regulation of intracellular ROS levels by reduction of H$_2$O$_2$. Excess amounts of H$_2$O$_2$ are known to cause oxidative damages to the host cells. H$_2$O$_2$ usually acts as signaling molecules in programmed cell death (PCD) under environmental stresses as well as in response to pathogen invasions (Qin et al., 2008; Mittler et al., 2004).

Reactive oxygen species, such as H$_2$O$_2$ play a central role in the activation of pathogen-induced PCD in plants. Findings suggest pathogen-induced PCD in tobacco is accompanied by the suppression of APX expression and reduction in cell capability to scavenge H$_2$O$_2$ so accumulation of H$_2$O$_2$ and the acceleration of PCD occurs (Mittler et al., 1998). In DND reaction in this study we observed that up regulation in APX expression and H$_2$O$_2$ levels wasn’t sufficient for cell death. Level and timing of H$_2$O$_2$ production in tobacco cells are critical points for APX regulation (de Pinto et al., 2006) and it seems that level of H$_2$O$_2$ production increases before appearance of necrosis symptom, so antioxidant defense systems such as APX activity protect plant against damage of oxidative stress (Sarowar et al., 2005).

Abscisic acid (ABA) response elements (TF11) are significant in plant response against abiotic and biotic stresses and ROS production (Mahalingam et al., 2003; Sarowar et al., 2005; Pei et al., 2000). Over production of ABA response elements in the promoters of differentially expressed genes in stress conditions may reflect crosstalk among stress signaling pathway mediated by messengers like H$_2$O$_2$ (Mahalingam et al., 2003).

Putative ML domain protein (TF13) belonging to the ML domain family is implicated in lipid recognition, particularly in the recognition of pathogen related products. These domain proteins are predicted to mediate diverse biological functions through interaction with specific lipids. (Marchler-Bauer et al., 2011).

The Radical-induced Cell Death1 (TE3) protein is a key regulator of several ROS and abiotic stress-related responses and it interacts

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**Table 2** Functional annotation of transcript derived fragments (TDFs) obtained by cDNA-AFLP in tobacco-*Ralstonia solanacearum* interaction.

<table>
<thead>
<tr>
<th>TDF</th>
<th>Length (bp)</th>
<th>Annotation</th>
<th>E-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>TE1</td>
<td>154</td>
<td>Hypothetical protein</td>
<td>6e-49</td>
</tr>
<tr>
<td>TE2</td>
<td>138</td>
<td>Ascorbate peroxidase</td>
<td>1e-27</td>
</tr>
<tr>
<td>TE3</td>
<td>101</td>
<td>Radical induced cell death 1 (RCD1)-like cell differentiation protein</td>
<td>8e-40</td>
</tr>
<tr>
<td>TE4</td>
<td>127</td>
<td>Plastid lipid associated protein</td>
<td>6e-54</td>
</tr>
<tr>
<td>TE5</td>
<td>159</td>
<td>Predicted protein Wax2 like</td>
<td>8e-35</td>
</tr>
<tr>
<td>TE6</td>
<td>154</td>
<td>Metal-dependent protein hydrolase</td>
<td>9e-50</td>
</tr>
<tr>
<td>TE8</td>
<td>159</td>
<td>Sesquiterpene synthase 1</td>
<td>3e-62</td>
</tr>
<tr>
<td>TE9</td>
<td>79</td>
<td>GEM-like protein 4</td>
<td>7e-17</td>
</tr>
<tr>
<td>TF10</td>
<td>117</td>
<td>Arv9/cf-9 rapidly elicited protein 140</td>
<td>6e-50</td>
</tr>
<tr>
<td>TF11</td>
<td>115</td>
<td>ABA response elements</td>
<td>3e-41</td>
</tr>
<tr>
<td>TF13</td>
<td>105</td>
<td>putative ML domain protein</td>
<td>6e-43</td>
</tr>
</tbody>
</table>
with several transcription factors (Jaspers et al., 2010). It displayed an enhanced cell death phenotype during incompatible interaction with the bacterial pathogen *Pseudomonas syringae* strain DC3000 (Overmyer et al. 2000a, b). Plants lacking this protein function display pleiotropic phenotypes including sensitivity to apoplastic ROS and salt, ultraviolet B and early flowering and senescence (Jaspers et al., 2010).

Avr9/Cf-9 rapidly elicited (TF10) genes are predicted to encode regulatory proteins, including protein kinases and transcription factors (Baulcombe, 1999). Many of the Avr9/Cf-9 rapidly elicited genes encode putative signaling components and thus may play pivotal roles in the initial development of the defense response (Rowland et al., 2005).

Wax2 (TE5) has a metabolic function associated with both cuticle membrane and wax synthesis (Chen et al., 2003). Waxes are major constituents of the cuticle and play important roles in plant defenses against bacterial and fungal pathogens (Jenks et al., 1994). Cutin and cuticular wax provide a physical barrier to pathogen ingress as the primary line of defense (Riederer, 2006).

Sesquiterpene synthases (TE8) are protein families which catalyze the conversion of sesquiterpene compounds in various plant species according to the demand and the environment (Kessler and Baldwin, 2001).

Induced sesquiterpenes can also form secondary chemical defenses (Bohlmann et al., 1998) and be involved in plant reproductive systems by protecting against any attacks of insects, bacteria and fungi (Dorothea et al., 2005). 12-15 copies of sesquiterpene synthase are found in the tobacco genome. It is also possible that these genes are regulated in response to the environment (Facchin and Chappell, 1992).

Our data support the hypothesis that DND phenotype in tobacco has some similarity especially in signaling process to more specific mechanism associated with induction of the hypersensitive reaction and it is distinct from general defense mechanisms.

Finally understanding the molecular basis of *R. solanacearum*-plant interactions by isolation and characterization of genes which are regulated in compatible or incompatible combinations could be useful for control of *R. solanacearum* by genetic engineering and breeding resistant cultivars. The bacterial wilt resistance is generally under polygenic control, while the control of resistance in *A. thaliana* is monogenic (Ishihiara et al., 2012). Research shows that interfamily transfer of R genes can provide a new strategy to develop pathogen-resistant crops (Narusaka et al., 2013) and Quantitative resistance information could be used for generating markers for the breeding of resistant cultivars.

References


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J. Crop Prot.


آنالیز ترانسفروم توتوون در واکنش به آلودگی رالسنویا سولاناکاروم

کیری مسلمخانی، جواد مظفری ۱، مسعود شمسبخش ۲ و ابراهیم محمدی گل‌تیه ۳

چکیده: یکی از بهترین استراتژی‌ها برای کنترل بیماری پژمرده‌ای با عامل استفاده از ارقام مقاوم اصلاح شده است. کسب اطلاعات در زمینه بیان ژن‌های دفاعی باعث ایجاد تغییرات جدید در تولید مقاومت گیاه عليه پاپزن‌ها می‌شود. تحقیق حاضر با استفاده از روش cDNA-AFLP به مطالعه بیان ژن‌های آنتی‌بیوتیک در واکنش دفاعی آزمونی Ralstonia solanacearum با بهره‌گیری از روش TD فرآیند انجام شد. در این روش با استفاده از R. solanacearum در گیاه توتوون، در فاصله زمانی ۰، ۲۴، ۴۸ و ۷۲ ساعت پس از آلوده‌سازی بین منفاوت‌ها و دفاعی‌ها شناسایی و از آنها فرآیند TD در توتوون خصوصاً در فرآیند دفاعی تغییرات دفاعی در واکنش وSENT از DND مکانیسم دفاعی عضوی در گیاه است.

واژگان کلیدی: توتوون، Ralstonia solanacearum ترانسفروم و تعامل